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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/737,246

DATE: 10/04/2001

TIME: 17:18:13

Input Set : A:\-3-1-1.app

Output Set: N:\CRF3\10042001\I737246.raw

3 <110> APPLICANT: Lu, Peter
4 Garman, Jonathan David
5 Candia III, Albert Frederick
6 Arbor Vita Corporation
8 <120> TITLE OF INVENTION: CLASP-3 Transmembrane Protein
10 <130> FILE REFERENCE: 020054-000311US
12 <140> CURRENT APPLICATION NUMBER: US 09/737,246
C--> 13 <141> CURRENT FILING DATE: 2001-09-20
15 <150> PRIOR APPLICATION NUMBER: US 60/160,860
16 <151> PRIOR FILING DATE: 1999-10-21
18 <150> PRIOR APPLICATION NUMBER: US 60/162,498
19 <151> PRIOR FILING DATE: 1999-10-29
21 <150> PRIOR APPLICATION NUMBER: US 60/170,453
22 <151> PRIOR FILING DATE: 1999-12-13
24 <150> PRIOR APPLICATION NUMBER: US 60/176,195
25 <151> PRIOR FILING DATE: 2000-01-14
27 <150> PRIOR APPLICATION NUMBER: US 60/182,296
28 <151> PRIOR FILING DATE: 2000-02-14
30 <150> PRIOR APPLICATION NUMBER: US 09/547,276
31 <151> PRIOR FILING DATE: 2000-04-11
33 <150> PRIOR APPLICATION NUMBER: US 60/196,267
34 <151> PRIOR FILING DATE: 2000-04-11
36 <150> PRIOR APPLICATION NUMBER: US 60/196,460
37 <151> PRIOR FILING DATE: 2000-04-11
39 <150> PRIOR APPLICATION NUMBER: US 60/196,527
40 <151> PRIOR FILING DATE: 2000-04-11
42 <150> PRIOR APPLICATION NUMBER: US 60/196,528
43 <151> PRIOR FILING DATE: 2000-04-11
45 <150> PRIOR APPLICATION NUMBER: US 09/687,837
46 <151> PRIOR FILING DATE: 2000-10-13
48 <150> PRIOR APPLICATION NUMBER: US 60/240,503
49 <151> PRIOR FILING DATE: 2000-10-13
51 <150> PRIOR APPLICATION NUMBER: US 60/240,508
52 <151> PRIOR FILING DATE: 2000-10-13
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55 <151> PRIOR FILING DATE: 2000-10-13
57 <150> PRIOR APPLICATION NUMBER: US 60/240,543
58 <151> PRIOR FILING DATE: 2000-10-13
60 <160> NUMBER OF SEQ ID NOS: 148
62 <170> SOFTWARE: PatentIn Ver. 2.1
64 <210> SEQ ID NO: 1
65 <211> LENGTH: 6828
66 <212> TYPE: DNA
67 <213> ORGANISM: Homo sapiens
69 <220> FEATURE:
70 <223> OTHER INFORMATION: full-length human CLASP-3 cDNA
72 <220> FEATURE:

ENTERED

p. 5

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75 <223> OTHER INFORMATION: human CLASP-3
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79                               Met Ala Glu Arg Arg Ala Phe Ala Gln Lys
80                               1           5           10
82 atc agc aga acg gtg gca gcc gaa gtt agg aag cag atc tcc gga caa 99
83 Ile Ser Arg Thr Val Ala Ala Glu Val Arg Lys Gln Ile Ser Gly Gln
84                               15           20           25
86 tat agt ggt tct ccc caa ctg ctc aaa aac ctt aat att gtt ggc aat 147
87 Tyr Ser Gly Ser Pro Gln Leu Leu Lys Asn Leu Asn Ile Val Gly Asn
88                               30           35           40
90 ata tcc cat cac acc aca gtg ccc ctt acc gaa gca gta gat cca gtg 195
91 Ile Ser His His Thr Thr Val Pro Leu Thr Glu Ala Val Asp Pro Val
92                               45           50           55
94 gat ttg gaa gat tac ctc att act cat cct ttg gct gtg gat tct ggg 243
95 Asp Leu Glu Asp Tyr Leu Ile Thr His Pro Leu Ala Val Asp Ser Gly
96                               60           65           70
98 cct tta cgg gat ttg att gaa ttt cct cca gat gat att gaa gtt gtt 291
99 Pro Leu Arg Asp Leu Ile Glu Phe Pro Pro Asp Asp Ile Glu Val Val
100 75           80           85           90
102 tat agt cct cgg gac tgc aga act ctt gtt tca gct gta cct gaa gaa 339
103 Tyr Ser Pro Arg Asp Cys Arg Thr Leu Val Ser Ala Val Pro Glu Glu
104                               95           100          105
106 agt gaa atg gat cca cat gtt aga gac tgt ata aga agt tat aca gaa 387
107 Ser Glu Met Asp Pro His Val Arg Asp Cys Ile Arg Ser Tyr Thr Glu
108                               110          115          120
110 gac tgg gca att gtc atc aga aaa tat cat aaa ttg gga aca gga ttt 435
111 Asp Trp Ala Ile Val Ile Arg Lys Tyr His Lys Leu Gly Thr Gly Phe
112                               125          130          135
114 aat ccc aat aca tta gat aaa cag aaa gaa agg caa aaa ggt ttg cca 483
115 Asn Pro Asn Thr Leu Asp Lys Gln Lys Glu Arg Gln Lys Gly Leu Pro
116                               140          145          150
118 aaa caa gtt ttt gaa tct gat gaa gct cca gat ggc aac agc tac cag 531
119 Lys Gln Val Phe Glu Ser Asp Glu Ala Pro Asp Gly Asn Ser Tyr Gln
120 155          160          165          170
122 gat gat caa gat gac ctt aaa aga cgt tca atg tca ata gat gat acc 579
123 Asp Asp Gln Asp Asp Leu Lys Arg Arg Ser Met Ser Ile Asp Asp Thr
124                               175          180          185
126 cca agg ggt agc tgg gcc tgt agt atc ttt gac ttg aaa aat tca ctt 627
127 Pro Arg Gly Ser Trp Ala Cys Ser Ile Phe Asp Leu Lys Asn Ser Leu
128                               190          195          200
130 cct gat gct ttg ctt ccc aat tta ctt gat cga act cca aat gaa gaa 675
131 Pro Asp Ala Leu Leu Pro Asn Leu Leu Asp Arg Thr Pro Asn Glu Glu
132                               205          210          215
134 ata gac cgt cag aat gat gac caa agg aaa tca aac cgt cac aaa gaa 723
135 Ile Asp Arg Gln Asn Asp Asp Gln Arg Lys Ser Asn Arg His Lys Glu
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139	Leu	Phe	Ala	Leu	His	Pro	Ser	Pro	Asp	Glu	Glu	Glu	Pro	Ile	Glu	Arg	
140	235					240					245					250	
142	ctt	agt	gtt	cct	gat	ata	ccc	aaa	gaa	cat	ttt	ggt	caa	aga	ctt	ctt	819
143	Leu	Ser	Val	Pro	Asp	Ile	Pro	Lys	Glu	His	Phe	Gly	Gln	Arg	Leu	Leu	
144					255					260						265	
146	gta	aaa	tgc	tta	tca	ctc	aag	ttt	gaa	att	gaa	att	gaa	ccc	att	ttt	867
147	Val	Lys	Cys	Leu	Ser	Leu	Lys	Phe	Glu	Ile	Glu	Ile	Glu	Pro	Ile	Phe	
148				270					275					280			
150	gca	agt	ttg	gct	tta	tat	gat	gtc	aag	gaa	aag	aaa	aag	att	tca	gaa	915
151	Ala	Ser	Leu	Ala	Leu	Tyr	Asp	Val	Lys	Glu	Lys	Lys	Lys	Ile	Ser	Glu	
152			285					290					295				
154	aac	ttt	tat	ttt	gac	ctt	aat	tct	gag	cag	atg	aaa	ggg	ttg	tta	cgt	963
155	Asn	Phe	Tyr	Phe	Asp	Leu	Asn	Ser	Glu	Gln	Met	Lys	Gly	Leu	Leu	Arg	
156		300					305					310					
158	cca	cat	gta	cca	cct	gct	gcc	att	act	acc	ctg	gca	aga	tca	gca	att	1011
159	Pro	His	Val	Pro	Pro	Ala	Ala	Ile	Thr	Thr	Leu	Ala	Arg	Ser	Ala	Ile	
160	315					320					325					330	
162	ttt	tct	atc	act	tat	cct	tcc	caa	gat	gtt	ttt	ctt	gta	ata	aag	cta	1059
163	Phe	Ser	Ile	Thr	Tyr	Pro	Ser	Gln	Asp	Val	Phe	Leu	Val	Ile	Lys	Leu	
164				335					340						345		
166	gaa	aaa	gtc	cta	cag	caa	gga	gac	att	gga	gag	tgt	gca	gaa	cca	tat	1107
167	Glu	Lys	Val	Leu	Gln	Gln	Gly	Asp	Ile	Gly	Glu	Cys	Ala	Glu	Pro	Tyr	
168			350					355					360				
170	atg	att	ttc	aaa	gaa	gca	gat	gcc	acc	aag	aat	aaa	gaa	aaa	ctg	gag	1155
171	Met	Ile	Phe	Lys	Glu	Ala	Asp	Ala	Thr	Lys	Asn	Lys	Glu	Lys	Leu	Glu	
172			365				370					375					
174	aaa	ctg	aag	agt	caa	gca	gat	cag	ttt	tgc	caa	aga	ctt	ggg	aaa	tat	1203
175	Lys	Leu	Lys	Ser	Gln	Ala	Asp	Gln	Phe	Cys	Gln	Arg	Leu	Gly	Lys	Tyr	
176		380					385				390						
178	cgc	atg	cct	ttt	gct	tgg	act	gca	atc	cat	tta	atg	aat	att	gtt	agc	1251
179	Arg	Met	Pro	Phe	Ala	Trp	Thr	Ala	Ile	His	Leu	Met	Asn	Ile	Val	Ser	
180	395					400					405					410	
182	agt	gct	ggg	agt	ttg	gaa	aga	gat	tct	aca	gaa	gta	gaa	atc	agt	act	1299
183	Ser	Ala	Gly	Ser	Leu	Glu	Arg	Asp	Ser	Thr	Glu	Val	Glu	Ile	Ser	Thr	
184				415					420						425		
186	gga	gaa	cga	aaa	ggg	tct	tgg	tca	gag	agg	agg	aat	tct	agt	att	gtt	1347
187	Gly	Glu	Arg	Lys	Gly	Ser	Trp	Ser	Glu	Arg	Arg	Asn	Ser	Ser	Ile	Val	
188			430						435				440				
190	ggc	aga	cga	tca	ctt	gaa	agg	aca	aca	agt	gga	gat	gat	gct	tgt	aac	1395
191	Gly	Arg	Arg	Ser	Leu	Glu	Arg	Thr	Thr	Ser	Gly	Asp	Asp	Ala	Cys	Asn	
192			445					450					455				
194	ttg	acg	agc	ttt	cga	cca	gct	act	ctc	aca	gtg	aca	aat	ttt	ttt	aag	1443
195	Leu	Thr	Ser	Phe	Arg	Pro	Ala	Thr	Leu	Thr	Val	Thr	Asn	Phe	Phe	Lys	
196		460					465					470					
198	cag	gaa	gga	gac	cgc	tta	agt	gat	gaa	gat	ctc	tac	aaa	ttc	ctt	gct	1491
199	Gln	Glu	Gly	Asp	Arg	Leu	Ser	Asp	Glu	Asp	Leu	Tyr	Lys	Phe	Leu	Ala	
200	475					480					485					490	
202	gat	atg	aga	agg	cca	tct	tct	gtc	tta	cgg	cga	cta	aga	cct	att	aca	1539

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203	Asp	Met	Arg	Arg	Pro	Ser	Ser	Val	Leu	Arg	Arg	Leu	Arg	Pro	Ile	Thr	
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206	gct	cag	ctc	aag	ata	gac	att	tct	ccc	gca	cct	gaa	aat	ccc	cat	tat	1587
207	Ala	Gln	Leu	Lys	Ile	Asp	Ile	Ser	Pro	Ala	Pro	Glu	Asn	Pro	His	Tyr	
208				510					515					520			
210	tgc	cta	act	ccg	gag	ctg	ctt	caa	gtg	aag	ctt	tac	cct	gac	agt	aga	1635
211	Cys	Leu	Thr	Pro	Glu	Leu	Leu	Gln	Val	Lys	Leu	Tyr	Pro	Asp	Ser	Arg	
212			525					530					535				
214	gtt	aga	cct	acc	aga	gaa	atc	tta	gag	ttt	ccc	gca	agg	gat	gtt	tat	1683
215	Val	Arg	Pro	Thr	Arg	Glu	Ile	Leu	Glu	Phe	Pro	Ala	Arg	Asp	Val	Tyr	
216		540					545				550						
218	gtt	cca	aac	act	act	tac	aga	aat	ctt	ctc	tac	ata	tac	cct	cag	agt	1731
219	Val	Pro	Asn	Thr	Thr	Tyr	Arg	Asn	Leu	Leu	Tyr	Ile	Tyr	Pro	Gln	Ser	
220	555					560				565					570		
222	ctt	aat	ttt	gcc	aat	cgt	caa	ggc	tct	gct	aga	aat	ata	aca	gtg	aaa	1779
223	Leu	Asn	Phe	Ala	Asn	Arg	Gln	Gly	Ser	Ala	Arg	Asn	Ile	Thr	Val	Lys	
224					575				580						585		
226	gtc	cag	ttt	atg	tat	gga	gag	gat	cca	agc	aat	gcc	atg	ccg	gta	atc	1827
227	Val	Gln	Phe	Met	Tyr	Gly	Glu	Asp	Pro	Ser	Asn	Ala	Met	Pro	Val	Ile	
228				590					595					600			
230	ttt	ggt	aaa	tct	agc	tgt	tca	gaa	ttt	tca	aag	gaa	gcc	tat	aca	gcc	1875
231	Phe	Gly	Lys	Ser	Ser	Cys	Ser	Glu	Phe	Ser	Lys	Glu	Ala	Tyr	Thr	Ala	
232			605					610					615				
234	gta	gta	tat	cat	aac	agg	tct	cct	gat	ttt	cat	gaa	gaa	atc	aag	gtt	1923
235	Val	Val	Tyr	His	Asn	Arg	Ser	Pro	Asp	Phe	His	Glu	Glu	Ile	Lys	Val	
236		620					625				630						
238	aag	ctt	cct	gct	act	tta	act	gac	cat	cat	cac	ttg	ctt	ttt	act	ttt	1971
239	Lys	Leu	Pro	Ala	Thr	Leu	Thr	Asp	His	His	His	Leu	Leu	Phe	Thr	Phe	
240	635					640				645					650		
242	tat	cat	gtt	agt	tgt	caa	caa	aaa	caa	aat	act	cct	ctt	gaa	aca	cca	2019
243	Tyr	His	Val	Ser	Cys	Gln	Gln	Lys	Gln	Asn	Thr	Pro	Leu	Glu	Thr	Pro	
244					655				660					665			
246	gtt	gga	tat	aca	tgg	ata	cca	atg	ctt	cag	aat	gga	cgg	ttg	aag	act	2067
247	Val	Gly	Tyr	Thr	Trp	Ile	Pro	Met	Leu	Gln	Asn	Gly	Arg	Leu	Lys	Thr	
248				670					675					680			
250	ggc	cag	ttt	tgc	ttg	cca	gtc	tca	ttg	gaa	aaa	cca	cca	cag	gct	tat	2115
251	Gly	Gln	Phe	Cys	Leu	Pro	Val	Ser	Leu	Glu	Lys	Pro	Pro	Gln	Ala	Tyr	
252			685					690					695				
254	tct	gta	ctg	tct	cct	gag	gtt	cct	cta	cct	ggc	atg	aaa	tgg	gta	gat	2163
255	Ser	Val	Leu	Ser	Pro	Glu	Val	Pro	Leu	Pro	Gly	Met	Lys	Trp	Val	Asp	
256		700					705				710						
258	aat	cac	aaa	ggt	gtt	ttt	aat	gtt	gaa	gtt	gtt	gct	gtt	tcg	tct	atc	2211
259	Asn	His	Lys	Gly	Val	Phe	Asn	Val	Glu	Val	Val	Ala	Val	Ser	Ser	Ile	
260	715					720				725						730	
262	cat	aca	caa	gat	cct	tat	ctt	gac	aaa	ttt	ttt	gct	ctg	gtc	aat	gct	2259
263	His	Thr	Gln	Asp	Pro	Tyr	Leu	Asp	Lys	Phe	Phe	Ala	Leu	Val	Asn	Ala	
264					735				740						745		
266	ctg	gat	gaa	cac	ctg	ttc	cca	gtc	cga	att	ggg	gac	atg	cga	atc	atg	2307
267	Leu	Asp	Glu	His	Leu	Phe	Pro	Val	Arg	Ile	Gly	Asp	Met	Arg	Ile	Met	

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270	gaa aat aac tta gaa aat gaa ttg aag agc agt att tca gca ctg aat	2355		
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272	765	770	775	
274	tca tcc cag ctg gaa cca gtg gtc cga ttt ctt cat ctt ctg cta gat	2403		
275	Ser Ser Gln Leu Glu Pro Val Val Arg Phe Leu His Leu Leu Leu Asp			
276	780	785	790	
278	aaa ctg ata ctt tta gtt att aga cct cct gtc att gct ggc caa ata	2451		
279	Lys Leu Ile Leu Leu Val Ile Arg Pro Pro Val Ile Ala Gly Gln Ile			
280	795	800	805	810
282	gtt aac cta ggt caa gca tct ttt gaa gcc atg gca tca att ata aat	2499		
283	Val Asn Leu Gly Gln Ala Ser Phe Glu Ala Met Ala Ser Ile Ile Asn			
284	815	820	825	
286	cga ctt cac aaa aac ttg gaa gga aat cat gac cag cat ggc aga aac	2547		
287	Arg Leu His Lys Asn Leu Glu Gly Asn His Asp Gln His Gly Arg Asn			
288	830	835	840	
290	agc ctt ctt gca tca tat att cat tat gtt ttc cgc cta cca aat act	2595		
291	Ser Leu Leu Ala Ser Tyr Ile His Tyr Val Phe Arg Leu Pro Asn Thr			
292	845	850	855	
294	tac cct aat tca tca tca cca ggt cct ggg ggt ttg gga gga tca gtg	2643		
295	Tyr Pro Asn Ser Ser Ser Pro Gly Pro Gly Gly Leu Gly Gly Ser Val			
296	860	865	870	
298	cat tat gcc aca atg gct aga tct gcg gtg aga cct gca agc ctt aat	2691		
299	His Tyr Ala Thr Met Ala Arg Ser Ala Val Arg Pro Ala Ser Leu Asn			
300	875	880	885	890
302	tta aat cgt tct cga agc ctt agt aat agc aat cca gat ata tct ggg	2739		
303	Leu Asn Arg Ser Arg Ser Leu Ser Asn Ser Asn Pro Asp Ile Ser Gly			
304	895	900	905	
306	act ccc acg tca cca gat gat gaa gtt cga tca atc atc ggg agt aag	2787		
307	Thr Pro Thr Ser Pro Asp Asp Glu Val Arg Ser Ile Ile Gly Ser Lys			
308	910	915	920	
310	ggt tta gat cgc tcc aat tcc tgg gtt aac act ggt ggt cca aaa gct	2835		
311	Gly Leu Asp Arg Ser Asn Ser Trp Val Asn Thr Gly Gly Pro Lys Ala			
312	925	930	935	
314	gcc cca tgg gga tcc aac ccc agt cca agt gca gaa tca aca cag gct	2883		
315	Ala Pro Trp Gly Ser Asn Pro Ser Pro Ser Ala Glu Ser Thr Gln Ala			
316	940	945	950	
318	atg gat cga agt tgt aat cgt atg tct tcg cac aca gag acg tca agt	2931		
319	Met Asp Arg Ser Cys Asn Arg Met Ser Ser His Thr Glu Thr Ser Ser			
320	955	960	965	970
322	ttc tta caa aca tta acg gga cgc tta cca act aaa aag ctt ttt cac	2979		
323	Phe Leu Gln Thr Leu Thr Gly Arg Leu Pro Thr Lys Lys Leu Phe His			
324	975	980	985	
326	gag gag ctg gct ttg cag tgg gtt gtt tgc agt ggc agc gtt cgg gaa	3027		
327	Glu Glu Leu Ala Leu Gln Trp Val Val Cys Ser Gly Ser Val Arg Glu			
328	990	995	1000	
330	tca gct ttg caa caa gcc tgg ttc ttt ttt gaa tta atg gta aag agc	3075		
331	Ser Ala Leu Gln Gln Ala Trp Phe Phe Phe Glu Leu Met Val Lys Ser			
332	1005	1010	1015	

Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

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Input Set : A:\-3-1-1.app

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L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1029 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (3) SEQUENCE:
L:1035 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (4) SEQUENCE:
L:1041 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (5) SEQUENCE:
L:1047 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (6) SEQUENCE:
L:4725 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:61
L:4726 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:61
L:4727 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:61
L:4728 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:61
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L:4820 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:64
L:4821 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:64
L:4822 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:64
L:4823 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:64
L:4824 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:64
L:4854 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:65
L:4880 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66
L:4881 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66
L:4883 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66
L:4884 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66
L:4885 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66
L:4886 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66
L:4887 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/737,246

DATE: 10/04/2001

TIME: 17:18:14

Input Set : A:\-3-1-1.app

Output Set: N:\CRF3\10042001\I737246.raw

L:4906 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:67
L:4909 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:67
L:4910 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:67
L:4911 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:67
L:4912 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:67
L:4913 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:67
L:4914 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:67
L:8028 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (105) SEQUENCE:
L:8034 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (106) SEQUENCE:
L:8040 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (107) SEQUENCE:
L:8046 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (108) SEQUENCE:
L:8052 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (109) SEQUENCE:
L:8058 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (110) SEQUENCE:
L:8064 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (111) SEQUENCE:
L:8070 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (112) SEQUENCE:
L:8076 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (113) SEQUENCE:
L:8082 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (114) SEQUENCE:
L:8088 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (115) SEQUENCE:
L:8094 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (116) SEQUENCE:
L:8100 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (117) SEQUENCE:
L:8106 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (118) SEQUENCE:
L:8112 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (119) SEQUENCE:
L:8118 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (120) SEQUENCE:
L:8124 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (121) SEQUENCE:
L:8130 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (122) SEQUENCE:
L:8136 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (123) SEQUENCE:
L:8142 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (124) SEQUENCE:
L:8148 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (125) SEQUENCE: